



RAW SEQUENCE LISTING **ERROR REPORT**

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Application Serial Number: 09/786,880

Source: OIPE

Date Processed by STIC: 8/15/2001

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

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Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/786,880

DATE: 08/15/2001

TIME: 08:37:31

Input Set : A:\16655PC1.APP.txt

Output Set: N:\CRF3\08132001\I786880.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: AVENTIS PHARMA S.A.
 5 <120> TITLE OF INVENTION: ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
 6 SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES
 8 <130> FILE REFERENCE: 16655
 10 <140> CURRENT APPLICATION NUMBER: US/09/786,880
 11 <141> CURRENT FILING DATE: 2001-03-08
 13 <150> PRIOR APPLICATION NUMBER: EP98402255.8
 14 <151> PRIOR FILING DATE: 1998-09-11
 16 <160> NUMBER OF SEQ ID NOS: 25
 18 <170> SOFTWARE: PatentIn Ver. 2.1

done
throughout

ERRORED SEQUENCES

1529 <210> SEQ ID NO: 11
 1530 <211> LENGTH: 1847
 1531 <212> TYPE: PRT
 1532 <213> ORGANISM: Candida albicans
 1534 <400> SEQUENCE: 11
 1535 Met Ser Gly Ile Phe Asn Trp Ser Leu Asp Val Phe Ala Asp Ile Tyr
 1536 1 5 10 15
 1538 Asn Thr Leu Lys Phe Glu Ser Asn Ile Asp Leu Asp Thr Ile Asp Phe
 1539 20 25 30
 1541 Thr Ser Ile Lys Asn Asp Leu Ala Asn Val Leu Ile Thr Pro Val Pro
 1542 35 40 45
 1544 Leu Asp Gln Ser Arg Ser Lys Leu Gly Asp Ala Ser Lys Pro Val Ala
 1545 50 55 60
 1547 Leu Pro Ser Gly Asp Glu Val Lys Leu Asn Gln Ala Ser Ile Glu Ile
 1548 65 70 75 80
 1550 Thr Gly Val Leu Ser Asn Glu Leu Asp Leu Asp Glu Leu Asn Thr Ala
 1551 85 90 95
 1553 Glu Leu Leu Tyr Asn Ala Ser Asp Leu Ser Tyr Lys Lys Gly Thr Ser
 1554 100 105 110
 1556 Ile Gly Asp Ser Ala Arg Leu Ala Tyr Tyr Leu Arg Ala His Tyr Ile
 1557 115 120 125
 1559 Leu Asn Ile Val Gly Tyr Leu Val Ser His Lys Arg Leu Asp Ile Ile
 1560 130 135 140
 1562 Thr Asn Asn Asn Gln Val Leu Phe Asp Asn Ile Leu Lys Ser Phe Ser
 1563 145 150 155 160
 1565 Lys Ile Tyr Thr Leu Ser Gly Lys Leu Asn Asp Met Ile Asp Lys Gln
 1566 165 170 175
 1568 Lys Val Thr Gly Asp Ile Asn Asn Leu Ala Phe Ile Asn Cys Ile Asn
 1569 180 185 190
 1571 Tyr Ser Arg Ser Gln Leu Phe Asn Ala His Glu Leu Leu Gly Gln Val
 1572 195 200 205
 1574 Val Phe Gly Leu Ala Asp Asn Tyr Tyr Glu Ser Tyr Gly Thr Leu Asn
 1575 210 215 220

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1577 Asn Tyr Asn Ser Leu Val Glu Phe Ile Leu Lys Asn Ile Ser Asp Glu
1578 225                230                235                240
1580 Asp Val Phe Val Ile His Phe Leu Pro Ser Thr Leu Gln Leu Phe Lys
1581                245                250                255
1583 Lys Leu Leu Gln Leu Gly Glu Glu Ser Leu Val Asp Gln Phe Tyr Lys
1584                260                265                270
1586 Thr Ile Thr Ser Ser Ile Leu Lys Asp Tyr Glu Ala Asn Asn Phe Ser
1587                275                280                285
1589 Lys Ser Glu Asp Ile Asp Leu Ser Lys Ser Lys Leu Ser Gly Phe Glu
1590                290                295                300
1592 Ile Val Thr Ser Phe Ile Phe Leu Thr Glu Phe Ile Pro Trp Cys Lys
1593 305                310                315                320
1595 Gln Leu Ser Ser Arg Thr Ala Lys Tyr Asp Phe Lys Asp Asp Ile Leu
1596                325                330                335
1598 Lys Tyr Met Glu Phe Leu Ile Ser Tyr Gly Val Met Glu Arg Leu Leu
1599                340                345                350
1601 Ser Tyr Cys Ser Glu Thr Ser Asn Ala Lys Thr Gln Gln Val Tyr Asp
1602                355                360                365
1604 Trp Ser Asn Met Tyr Asp Phe Arg Ala Leu Leu Gln Lys Asn Phe Pro
1605                370                375                380
1607 Arg Leu Thr Pro Ala Lys Phe His Tyr Pro Gly Asn Gln Glu Leu Leu
1608 385                390                395                400
1610 Asn Ala Val Arg Pro Gly Tyr Glu Asn Ile Ser Lys Leu Ile Asp Ile
1611                405                410                415
1613 Ser Phe Leu Thr Leu Asp Pro Ser Leu Asn Glu Thr Leu Val Ser Pro
1614                420                425                430
1616 Phe Phe Gln Ser Phe Phe Ser Val Phe Ile Ser Asn Ala Ala Val Val
1617                435                440                445
1619 Met Thr Ser Leu Arg Asp Ser Glu Glu Asp Phe Val Leu Ser Ser Leu
1620                450                455                460
1622 Asn Glu Ser Asp Glu Glu Glu Glu Glu Glu Ser Asp Ser Asp Glu
1623 465                470                475                480
1625 Asp Ser Ser Thr Pro Lys Asn Lys Glu Lys Ser Ala Gly Leu Asp Leu
1626                485                490                495
1628 Asp Lys Ile Ala Gln Arg Ala Glu Leu Glu Arg Phe Tyr Leu Ala Phe
1629                500                505                510
1631 Ala Tyr Thr Tyr Asn Asn Arg Pro Glu Leu Cys Ala Leu Phe Trp Gly
1632                515                520                525
1634 Asn Glu Gln Val Thr His Asp Ile Ile Gly Phe Ile Ser Trp Gly Leu
1635                530                535                540
1637 Ala Asn Asn Thr Ser Pro Leu Ile Thr Ala Thr Phe Cys Leu Leu Leu
1638 545                550                555                560
1640 Gly Ser Leu Ala Ser Ala Gly Ala Glu Ala Thr Ser Arg Ile Trp Glu
1641                565                570                575
1643 Ile Leu Val His Asn Asn Asn Ala Ser Thr Arg Lys Asn Asp Phe
1644                580                585                590
1646 Ser Lys Val Ser Val Asp Ser Leu Tyr Asp Ser Leu Lys Tyr Tyr Ile
1647                595                600                605
1649 Asp Ser Leu Asn Glu Ser Phe Glu Gln Asp Leu Asn Ala Gln Leu Met

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1650	610	615	620
1652	Leu Asn Gln Lys Lys Gln Asp Phe Leu Phe Ser Thr Thr Thr Ser Lys		
1653	625	630	635
1655	Gln Asp Leu Asp Asp Ser Gly Glu Asn Arg Ile Val Ile Glu Leu Ala		640
1656	645	650	655
1658	Glu Asp Ser Leu Val Leu Ile Ser Gly Phe Ile Gln Leu Leu Ser Ala		
1659	660	665	670
1661	Ile Val Lys Asn Leu Asn Thr Lys Asn Glu Arg Ser Lys Glu Ile Lys		
1662	675	680	685
1664	Ser Val Val Tyr Thr Arg Phe Ser Pro Ile Ile Lys Gly Phe Leu Lys		
1665	690	695	700
1667	Phe Asp Asn Leu Ile Asn Gly Ser Arg Phe Leu Gln Val Asp Ala Ser		
1668	705	710	715
1670	Ile Gln Ser Thr Asn Asn Pro Lys Phe Ile Asp Leu Pro Asn Val Phe		720
1671	725	730	735
1673	Val Ser Asp Asp Ser Arg Ile Ile Leu Thr Asn Leu Ile Leu Thr Phe		
1674	740	745	750
1676	Leu Gly Asp Phe Val Thr Asn Asp Ser Asp Pro Tyr Ile Arg Tyr Glu		
1677	755	760	765
1679	Ile Trp Arg Leu Val Asp Arg Trp Met Tyr Gln Gly Leu His Ser Leu		
1680	770	775	780
1682	Pro Glu Asp Lys Lys Asp Asp Ala Phe Arg His Ile Lys Arg Lys Tyr		
1683	785	790	795
1685	Asn Ser Lys Lys Asn Val Pro Ile Asn Gln Ala Phe Ser Thr Asn Leu		800
1686	805	810	815
1688	Thr His Leu Ser Gln Ile Gly Asn Phe Thr Val Leu Val Lys Lys Leu		
1689	820	825	830
1691	Leu Thr Pro Tyr Ala Asp Ser Asn Glu Ala Phe Thr Lys Tyr Ser Leu		
1692	835	840	845
1694	Leu Tyr Pro Cys Asp Leu Gly Leu Gly Tyr Arg Phe Asn Asn Gln Leu		
1695	850	855	860
1697	Gly Ile Trp Pro Tyr Ile Glu Phe Leu Met Gln Asn Val Phe Ala Asn		
1698	865	870	875
1700	Ser Gly Thr Ile Ala Asn Lys Arg Asp Arg Val Asn Leu Gln Leu Asn		880
1701	885	890	895
1703	Leu Leu Glu Leu Phe Ser Asn Ala Leu Gln Gly Val Asp Trp Lys Phe		
1704	900	905	910
1706	Leu Ile Asp Val Ala Pro Lys Ile Ile Arg Asp Leu Lys Asn Phe Asn		
1707	915	920	925
1709	Gly Ile Phe Asp Ser Leu Ile Pro Gly Val Gln Leu Asp Phe Glu Val		
1710	930	935	940
1712	Phe Val Lys Leu His His Ser Val Ala Val Ile Asn Tyr Leu Phe Glu		
1713	945	950	955
1715	Asn Arg Thr Phe Ser Ala Leu Phe Lys Leu Val Asn Ile Gly Val Asp		
1716	965	970	975
1718	Ser Val Asn Glu Ser Gly Glu Ser Ala Glu Leu Val Ser His Ala Leu		
1719	980	985	990
1721	Gly Leu Ile Asn Ser Leu Leu Arg Val Gln Asn Ser Phe Ile Asn Lys		
1722	995	1000	1005

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1724 Leu Leu Pro Ile Leu Arg Asn Lys Asp Thr Gln Gln Gln Leu His Arg
1725      1010      1015      1020
E--> 1727 Gly Thr Ala Ile Gly Ile Gly Thr Ser Met Ser Leu Ala Leu Ala Thr
      1728 025 1025      1030      1035      1040
1730 Pro Arg Thr Ile Phe Asp Cys Ile Tyr Tyr Pro Lys Asn Leu Gly Thr
1731      1045      1050      1055
1733 His Gly Val Ala Asp Phe Tyr Glu Val Ile Leu Phe His Leu Ser Ala
1734      1060      1065      1070
1736 Val Val Gln Phe Ala Leu Tyr Val Ser Cys Glu Asn Thr Ile Ser Asn
1737      1075      1080      1085
1739 Lys Ala Ile Ser Ile Leu Lys Gly Val Ser Gln Ser Lys Phe Phe Val
1740      1090      1095      1100
E--> 1742 Thr Arg Val Ser Ser Ser Ala Asp Pro Leu Leu Asn Asn Asp Arg Leu
      1743 105 1105      1110      1115      1120
1745 Ile Thr Thr Phe Glu Asn Ile Asp Glu Ser Ile Lys Ile Lys Phe Ala
1746      1125      1130      1135
1748 Phe Ile Asp Lys Phe Glu Glu Leu Glu Asp Ser Leu Asn Met Lys Tyr
1749      1140      1145      1150
1751 Glu Ile Leu Asp Phe Val Leu Gly Asn Leu Asn Gln Phe Asp Gly Lys
1752      1155      1160      1165
1754 Val Ala Thr Thr Ala His Phe Leu Leu Gly Tyr Lys Val Lys Gly Asp
1755      1170      1175      1180
1757 Thr Leu Asp Leu Val Gln Thr Asn Asp Gln Asn Thr Leu Leu Lys Ser
E--> 1758 185      1190      1195      1200
1760 Phe Leu Asn Thr Leu Ser Ile Ser Leu Asp Leu Ile Ser Glu Ile Asp
1761      1205      1210      1215
1763 Tyr Asn Asn Gly Asn Asn His Ile Ile Asp Val Gly Pro Ala Lys Leu
1764      1220      1225      1230
1766 Ser Ser Leu Ile Leu Gln Ile Leu Ile Lys Leu Cys Gln Asp Pro Ile
1767      1235      1240      1245
1769 Ser Ser Ser Ile Thr Leu Asn Gln Leu Arg Glu Tyr Glu Glu Leu Phe
1770      1250      1255      1260
1772 Gln Lys Leu Val Asn Cys Gln Pro Lys Leu Asp Leu Asn Thr Val Trp
E--> 1773 265      1270      1275      1280
1775 Cys Gly Asn Gln Phe Asp Gly Asp Leu Gln Ile Asp Ala Ser Asn Val
1776      1285      1290      1295
1778 Phe Val Asp Asn Gln Ala Ser Thr Gln Ala Phe Phe Ser Phe Ile Asn
1779      1300      1305      1310
1781 Gln Arg Asn Leu Ile Leu Gln Tyr Leu Ser Leu Glu Phe His Ser Val
1782      1315      1320      1325
1784 Lys Ser Arg Thr Lys Arg Glu Tyr Tyr Ser Lys Val Leu Thr Asn Asp
1785      1330      1335      1340
1787 Lys Glu Phe Val Asn Arg Thr Pro Lys Val Leu Thr Phe Leu Asn Ile
E--> 1788 345      1350      1355      1360
1790 Leu Asn Tyr Ser Phe Lys Asn Phe Glu Val Gln Lys Tyr Glu Trp Leu
1791      1365      1370      1375
1793 Asp Gln Lys Phe Asn Val Ser Leu Leu Leu Ala Glu Val Asn Ala Gln
1794      1380      1385      1390
1796 Lys Asn Gly Thr Leu Asp Phe Ser Val Leu Thr Lys Val Phe Arg Leu

```

When
numbering
the first
amino acid on
a line, begin
number under
first letter of
amino acid

e.g. Gly
1025

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```

1797          1395          1400          1405
1799 Leu Cys Gln Thr Ser Asn Leu Ile Thr Pro Glu Ser Lys Gln Leu Phe
1800          1410          1415          1420
1802 Ala Glu Glu Ile Met Val Glu Gly Ser Lys Ile Ser Asp Phe Val Thr
E--> 1803 425          1430          1435          1440
1805 Lys Tyr Leu Val Ser Thr Asp Leu Lys Asp Val Gln Leu Lys Cys Leu
1806          1445          1450          1455
1808 His Ser Trp Cys Gln Leu Ile Glu Ile Leu Val Thr Asp Ser Gly Ile
1809          1460          1465          1470
1811 Asn Ser Leu Asn Phe Ile Leu Glu Val Leu Gln Val Ile Ile Pro Lys
1812          1475          1480          1485
1814 Ile Asn Asp Tyr Phe Asp Val Asp Ile Leu Phe Ser Glu Glu Met Val
1815          1490          1495          1500
1817 Ser Leu Cys Val Leu Leu Phe Asp Leu Tyr Asp Gln Leu Thr Leu Ala
E--> 1818 505          1510          1515          1520
1820 Asp Arg Lys Gly Glu Asp Phe Ala Leu Gly Ile Glu Arg Leu Ile Pro
1821          1525          1530          1535
1823 Leu Phe Gln Thr Cys Ile Ala Gly Ile Leu Asn Ser Asn Ser Thr Pro
1824          1540          1545          1550
1826 Ser Leu Arg Ser Asp Leu Tyr Val Val Gly Asn Lys Phe Leu Leu Lys
1827          1555          1560          1565
1829 Cys Phe Glu Arg Glu Ser Phe Leu Lys Gln Val Met His Ile Ile Lys
1830          1570          1575          1580
1832 Ser Val Asp Lys Lys Phe Gln Val Ile Cys Asn Asp Ala Ile Tyr
E--> 1833 585          1590          1595          1600
1835 Ser Glu Gly Pro Ser Arg Ile Thr Ser Thr Leu Phe Leu Glu Ser Leu
1836          1605          1610          1615
1838 Val His Leu Gly Thr Leu Val Lys Val Asp Phe Ile Leu Asn Ala Leu
1839          1620          1625          1630
1841 Ile Lys Asn Asn Ala Leu Leu Leu Leu Val Arg Ser Val Lys Arg Thr
1842          1635          1640          1645
1844 Asp Ala Met Ile Lys Leu Cys Gln Glu Lys Asn Ser Gly Val Thr Leu
1845          1650          1655          1660
1847 Asp His Phe Ile Phe Asp Leu Met Ala Phe Lys Ala Thr Leu Tyr Phe
E--> 1848 665          1670          1675          1680
1850 Phe Val Arg Val Ala Lys Ser Lys Asn Gly Ala Leu Gln Leu Ile Gln
1851          1685          1690          1695
1853 Asn Glu Leu Phe Ser Ile Leu His Gln Ser Lys Phe Leu Gln Ile Asp
1854          1700          1705          1710
1856 Pro Asp Ile Gly Leu Ser Leu Arg Ile Glu Glu Val Gln Asp His Lys
1857          1715          1720          1725
1859 Thr Val Asn Val Asn Val Leu Leu Asp Thr Pro Leu Ser Ile Thr Asp
1860          1730          1735          1740
1862 Leu Val Asp Pro Tyr Lys Leu Arg Ser Glu Asn Thr Ile Ser Tyr Phe
E--> 1863 745          1750          1755          1760
1865 Glu Phe Leu Val Pro Ile Phe Gln Leu Leu Thr Thr Val Leu Leu Ser
1866          1765          1770          1775
1868 Met Gly Pro Asn Tyr Gln Pro Ala Ile Ile Gln Thr Arg Glu Leu Met
1869          1780          1785          1790

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1871 Lys Ser Val Asn Arg Leu Val Val Gly Val Met Lys Arg Asp Phe Leu
 1872 1795 1800 1805
 1874 Val Glu Thr Lys Gln Ile Gly Gln Gly Leu Tyr Lys Glu Glu Ser His
 1875 1810 1815 1820
 1877 Glu Leu Val Ser Leu Lys Glu Leu Val Lys Leu Phe Ile Leu Ile Asp
 E--> 1878 825 1830 1835 1840
 1880 Ser Leu Ala His Tyr Ser Val
 1881 1845
 3121 <210> SEQ ID NO: 21
 3122 <211> LENGTH: 1257
 3123 <212> TYPE: PRT
 3124 <213> ORGANISM: Candida albicans
 3126 <400> SEQUENCE: 21
 3127 Met Asp Ile Pro Pro Lys Pro Thr Leu Lys Ala Ile Lys Lys Phe Arg
 3128 1 5 10 15
 3130 Thr Leu Asp Glu Ile Lys Tyr Ala Met Lys His Val Phe Gln Asp Ala
 3131 20 25 30
 3133 Gln Leu Gly Leu Ala Gly His Arg Lys Leu Val Val Ile Leu Lys Asn
 3134 35 40 45
 3136 Val Phe Lys Lys Ala Ile Glu Leu Asn Gln Ile Asn Phe Phe Ala Met
 3137 50 55 60
 3139 Cys Phe Thr Lys Leu Leu Ser Lys Val Leu Pro Leu Lys Arg Gly Val
 3140 65 70 75 80
 3142 Leu Ala Gly Asp Arg Ile Val Lys Phe Cys Tyr Leu Phe Val Asn Gly
 3143 85 90 95
 3145 Leu Val Lys Asp Ala Asn Glu Glu Lys Arg Ser Lys Glu Glu Glu Lys
 3146 100 105 110
 3148 Glu Glu Lys Asp Lys Asp Glu Asp Lys Asp Thr Asn Glu Ser Asp Lys
 3149 115 120 125
 3151 Asn Glu Glu Asp Gln Glu Asp Gln Glu Gly Glu Gly Asp Gln Glu Thr
 3152 130 135 140
 3154 Pro Ile Ser Glu Phe Ile Ser Tyr Leu Ile Lys Tyr Leu Leu Ser Gly
 3155 145 150 155 160
 3157 Ile Glu Ala Lys Asp Lys Leu Val Arg Tyr Arg Val Val Gln Thr Leu
 3158 165 170 175
 3160 Ala Tyr Leu Val Glu Phe Leu Thr Glu Ile His Glu Asn Asn Thr Leu
 3161 180 185 190
 3163 Glu Ala Leu Tyr Thr Leu Leu Ser Asn Arg Leu Gln Asp Lys Glu Leu
 3164 195 200 205
 3166 Ser Ile Arg Ile Gln Ala Val Val Ala Leu Ser His Phe Gln Leu Phe
 3167 210 215 220
 3169 Glu Phe Ser Ile Glu Gly Asp Thr Gly Glu Phe Glu Asp Glu Leu Ile
 3170 225 230 235 240
 3172 Ser Ser Asn Gln Ile Gln Asn Lys Leu Ile Asn Ser Ile Gln Asn Asp
 3173 245 250 255
 3175 Asp Ser Pro Glu Val Arg Arg Ala Ala Leu Met Asn Leu Val Lys Thr
 3176 260 265 270
 3178 Gln Asp Thr Ile Pro Ile Leu Leu Glu Arg Ala Arg Asp Ser Asn Ser
 3179 275 280 285

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3181 Ile Asn Arg Arg Leu Val Tyr Ser Lys Ile Ala Arg Glu Leu Ile Thr
3182      290      295      300
3184 Asp Leu Asp Asp Leu Glu Phe Glu Asp Arg Glu Phe Leu Leu Lys Trp
3185 305      310      315      320
3187 Gly Leu Asn Asp Arg Asp Glu Thr Val Lys Ala Ala Ala Thr Lys Met
3188      325      330      335
3190 Leu Thr Ile Tyr Trp Tyr Gln Ser Val Asn Glu Asp Leu Leu Glu Leu
3191      340      345      350
3193 Ile Asp Gln Leu Asn Val Lys Ser Ala Ile Ala Glu Gln Ala Ile Leu
3194      355      360      365
3196 Ala Phe Phe Lys Asn Lys Pro Glu Val Leu Glu Thr Ile Lys Ile Asp
3197      370      375      380
3199 Glu Ser Tyr Trp Lys Asn Leu Thr Thr Glu Lys Ala Phe Leu Met Arg
3200 385      390      395      400
3202 Thr Phe Tyr Gln Tyr Cys Asn Glu Asn Gln Leu His Ala Leu Met Asp
3203      405      410      415
3205 Ala Asn Phe Pro Glu Leu Leu Asp Leu Ser Ile Thr Leu Glu Lys Tyr
3206      420      425      430
3208 Leu Ser Val Arg Leu Lys Thr Ile Asn Glu Asn Glu Asn Leu Val Lys
3209      435      440      445
3211 Thr Trp Glu Thr Tyr Asn Ala Lys Ile Asp Glu Leu Asp Asp Gln Ile
3212      450      455      460
3214 Phe Ser Leu Glu Asn Gln Ile Ser Arg Ile Asn Thr Asp Ala Asp Asn
3215 465      470      475      480
3217 Phe Arg Lys Ser Leu Ser Asn Ile Glu Glu Asp Ile Ile Glu Ile Asn
3218      485      490      495
3220 Ile Ala Lys Asp Leu Phe Lys Lys Arg Ile Lys Gln Leu Lys Asn Asn
3221      500      505      510
3223 Ser Gly Asn Leu Glu Asp Leu Ile Thr Glu Glu Asn Gln Glu Ile Ala
3224      515      520      525
3226 Asp Gln Ile Lys Asp Phe Leu Met Glu Asp Leu Gln Gln Gln Leu Glu
3227      530      535      540
3229 Asp Ile Asn Lys Asn Leu Asp Glu Ile Glu His His Pro Glu Asp Ile
3230 545      550      555      560
3232 Thr Ala Lys Leu Glu Glu Leu Gln Thr Lys Tyr Asp Ser Cys Ile Arg
3233      565      570      575
3235 Ala Leu Glu Thr Thr Ser Glu Leu Lys Ile Gln Thr Val Gln Ile Phe
3236      580      585      590
3238 Glu Gln Glu His Glu Asn Asp Cys Ile Pro Phe Val Asp Ala Leu Lys
3239      595      600      605
3241 Glu Leu Glu Phe Ile Ile Asn Gln Leu Leu Leu Ile Val Lys Asp Phe
3242      610      615      620
3244 Asp Tyr Gly Asp Glu Met Ala Arg Arg Lys Leu Leu His Ile Ile Arg
3245 625      630      635      640
3247 Met Thr Leu Thr Glu Asp Lys Leu Pro Asp Ala Leu Ile Ser Val Ala
3248      645      650      655
3250 Leu Arg Val Leu Arg Ala Leu Ser Ile Asn Glu Lys Asp Phe Val Ser
3251      660      665      670
3253 Met Ala Val Glu Ile Ile Thr Asp Ile Arg Asp Ser Arg Asp Asp Glu

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3254      675      680      685
3256 Glu Phe His Ser Ala Ala Ala Thr Phe Asp Asp Asp Asp Asp Ile
3257      690      695      700
3259 Leu Gly Asn Gly Asp Asp Glu Ser Gln Gln Ser Ser Leu Ser Ala
3260 705      710      715      720
3262 Val Thr Lys Lys Arg Arg Ile Glu Pro Asp Met Pro Pro Asp Asp Ile
3263      725      730      735
3265 Val Leu Arg Cys Leu Thr Met Thr Gln Tyr Val Leu Glu Val Ile Thr
3266      740      745      750
3268 His Ser Leu Asp Asp His Leu Ser Leu Ser Ser Ile Tyr Ser Gly Ile
3269      755      760      765
3271 Val Asn Tyr Ala Ile Gln Asn Glu Ser Lys Lys Lys Leu Tyr Leu Ala
3272      770      775      780
3274 Gly Leu Thr Cys Leu Gly Leu Tyr Ser Leu Ile Asp Ser Lys Ile Ala
3275 785      790      795      800
3277 Arg Ile Ala Thr Thr Thr Leu Leu Leu Ala Met Arg Ser Asn Gly Glu
3278      805      810      815
3280 Glu Val Lys Glu Ile Gly Met Lys Ala Ile Val Asp Ile Leu Ala Ile
3281      820      825      830
3283 Tyr Gly Met Ser Ile Leu Asp Lys Ser Ser Lys Tyr Lys Tyr Ser Arg
3284      835      840      845
3286 Met Phe Phe Lys Val Leu Asn Ser Phe Asp Ala Pro Lys Leu Gln Cys
3287      850      855      860
3289 Ile Val Ala Glu Gly Leu Cys Lys Leu Phe Leu Ala Asp Ile Leu Tyr
3290 865      870      875      880
3292 Lys Thr Asp Lys Arg Ser Leu Phe Gly Asn Ala Ile Gln Gly Gly Gly
3293      885      890      895
3295 Gly Gly Gly Gly Glu Asn Asp Asp Pro Thr Thr Thr Asn Asp Asp Glu
3296      900      905      910
3298 Thr Glu Glu Glu Thr Asp Arg Glu His Glu Lys His Leu Phe Glu Ala
3299      915      920      925
3301 Ile Val Leu Ile Tyr Phe Asn Pro Asn Thr Lys Ser Asn Gln Glu Leu
3302      930      935      940
3304 Gln Gln Ile Leu Ser Phe Cys Ile Pro Val Tyr Ala Phe Ser His Ile
3305 945      950      955      960
3307 Asn His Gln Ile Asn Leu Ala Ala Val Ser Gly Asp Val Ile Tyr Arg
3308      965      970      975
3310 Leu Phe Thr Glu Thr Glu Thr Glu Leu Ser Pro Ser Val Ile Ile Pro
3311      980      985      990
3313 Gln Leu Ile Ser Trp Cys Asp Pro Arg Asn Leu Val Lys Leu Ser Asn
3314      995      1000      1005
3316 Glu Glu Ile Asn Gln Ala Thr Ser His Leu Trp Gln Cys Val Tyr Leu
3317      1010      1015      1020
3319 Leu Gln Val Val Glu Gln Val Asp Ala Arg Asn Val Lys Arg Cys Ile
E--> 3320 1025/1025      1030      1035      1040
3322 Ile Asn Asn Leu Asn Lys Phe His Ile Thr Glu Glu Leu Glu Ser Asn
3323      1045      1050      1055
3325 Gln Leu Gln Ala Leu Ile Lys Ala Leu Asp Ala Thr Val Glu Leu Phe
3326      1060      1065      1070

```

RAW SEQUENCE LISTING

DATE: 08/15/2001

PATENT APPLICATION: US/09/786,880

TIME: 08:37:31

Input Set : A:\16655PC1.APP.txt

Output Set: N:\CRF3\08132001\I786880.raw

3328 Thr Asn Asn Glu Asp Asn Pro Asn Phe Ile Leu Asp Lys Pro Thr Lys
 3329 1075 1080 1085
 3331 Lys Asn Phe Asp Thr Phe Ile Glu Ser Ile Lys Asn Lys Leu Glu Ile
 3332 1090 1095 1100
 3334 Ala Gln Lys Arg Glu Glu Asn Glu Leu Ile Lys Ser Gly Thr Asn Ser
 E--> 3335 105 1110 1115 1120
 3337 Ile Leu His Glu Leu Asp Asp Leu Asp Ile Gly Thr Gly Glu Ser Ser
 3338 1125 1130 1135
 3340 Gln Ile Ser Ile Lys Ser Glu Thr Lys Arg Arg Asp Leu Asp Arg Ser
 3341 1140 1145 1150
 3343 Leu Gln Val Ser Lys Thr Thr Ser Pro Glu Thr Ser Glu Asn Glu Asp
 3344 1155 1160 1165
 3346 Glu Glu Asp Asp Asn Glu Glu Glu Glu Gln Glu Lys Lys Lys Ser Phe
 3347 1170 1175 1180
 3349 Thr Asp Gly Lys Asn Lys Leu Glu Leu Lys Ala Asp Lys Pro Ile Thr
 E--> 3350 185 1190 1195 1200
 3352 Phe Lys Ala Glu Asp Lys Arg Glu Gly Ser Val Glu Thr Asp His Gly
 3353 1205 1210 1215
 3355 Gln Glu Gln Val Leu Val Glu Ser Lys Lys Val Ile Asp Ser Asn Val
 3356 1220 1225 1230
 3358 Glu Asp Ser Leu Glu Asp Ile Asp Lys Phe Leu Glu Glu Ala Asp Asp
 3359 1235 1240 1245
 3361 Val Asp Tyr Gly Asp Ile Ser Met Asp
 3362 1250 1255
 3464 <210> SEQ ID NO: 25
 3465 <211> LENGTH: 231 910
 3466 <212> TYPE: DNA
 3467 <213> ORGANISM: Artificial Sequence
 3469 <220> FEATURE:
 3470 <223> OTHER INFORMATION: Description of Artificial Sequence: Homologous
 3471 Fragment to Sc YOR110
 3473 <400> SEQUENCE: 25
 3474 atatgtgttg atagttacac atgcagcaac gaaaattgct ttaggatcag ctttattaca 60
 3476 gttaaaatca gttactgatg ttatagatga taatcaaact gtgttacgtg ctggtgcatg 120
 3478 ttcattatcc aaatttgta gagatggcga agataaaacc aatcatacta ttcaatggaa 180
 3480 aattgtcatg aatggtaatt gtgaattctt gacacagggt gaagaaatga a 231
 E--> 3484 <aaa gag att gga atg aaa gct att gtg gat ata ttg gca att 2496 273
 3485 Glu Val Lys Glu Ile Gly Met Lys Ala Ile Val Asp Ile Leu Ala Ile
 W--> 3486 820 825 830
 E--> 3488 tat ggt atg agt att ctt gat aaa tca tct aaa tac aaa tat tca aga 2544
 3489 Tyr Gly Met Ser Ile Leu Asp Lys Ser Ser Lys Tyr Lys Tyr Ser Arg
 W--> 3490 835 840 845
 E--> 3492 atg ttt ttc aaa gtt tta aat tca ttt gat gca cca aaa tta caa tgc 2592
 3493 Met Phe Phe Lys Val Leu Asn Ser Phe Asp Ala Pro Lys Leu Gln Cys
 W--> 3494 850 855 860
 E--> 3496 att gtc gct gaa gga tta tgc aaa ttg ttt tta gcc gat att ttg tac 2640
 3497 Ile Val Ala Glu Gly Leu Cys Lys Leu Phe Leu Ala Asp Ile Leu Tyr
 W--> 3498 865 870 875 880
 E--> 3500 aag act gac aaa cgg agt tta ttt gga aat gct att caa ggt ggt ggt 2688

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 above
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 acid

has.
 off

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/786,880

DATE: 08/15/2001

TIME: 08:37:31

Input Set : A:\16655PC1.APP.txt

Output Set: N:\CRF3\08132001\I786880.raw

	3501	Lys	Thr	Asp	Lys	Arg	Ser	Leu	Phe	Gly	Asn	Ala	Ile	Gln	Gly	Gly	Gly	
W-->	3502					885				890					895			
E-->	3504	ggt	ggt	ggt	ggt	ggt	aat	gat	gat	cca	act	acc	acc	aat	gac	gat	gaa	2736
	3505	Gly	Gly	Gly	Gly	Gly	Asn	Asp	Asp	Pro	Thr	Thr	Thr	Asn	Asp	Asp	Glu	
W-->	3506					900				905					910			
E-->	3508	act	gaa	gaa	gaa	aca	gat	cga	gag	cat	gaa	aag	cat	tta	ttt	gaa	gcg	2784
	3509	Thr	Glu	Glu	Glu	Thr	Asp	Arg	Glu	His	Glu	Lys	His	Leu	Phe	Glu	Ala	
W-->	3510					915				920					925			
E-->	3512	att	gta	ctt	att	tat	ttc	aac	ccc	aac	acc	aaa	tca	aat	caa	gaa	tta	2832
	3513	Ile	Val	Leu	Ile	Tyr	Phe	Asn	Pro	Asn	Thr	Lys	Ser	Asn	Gln	Glu	Leu	
W-->	3514					930				935					940			
E-->	3516	caa	caa	att	ttg	tca	ttt	tgt	att	cca	gtt	tat	gcc	ttt	tct	cat	ata	2880
	3517	Gln	Gln	Ile	Leu	Ser	Phe	Cys	Ile	Pro	Val	Tyr	Ala	Phe	Ser	His	Ile	
W-->	3518					945				950					955			
E-->	3520	aat	cat	caa	atc	aat	tta	gct	gca	gtt	agt	ggt	gat	gtt	att	tat	cga	2928
	3521	Asn	His	Gln	Ile	Asn	Leu	Ala	Ala	Val	Ser	Gly	Asp	Val	Ile	Tyr	Arg	
W-->	3522					965				970					975			
E-->	3524	ctt	ttc	act	gaa	aca	gaa	aca	gaa	tta	tca	cca	agt	gtt	ata	atc	cct	2976
	3525	Leu	Phe	Thr	Glu	Thr	Glu	Thr	Glu	Leu	Ser	Pro	Ser	Val	Ile	Ile	Pro	
W-->	3526					980				985					990			
E-->	3528	caa	tta	ata	tca	tggt	tgt	gat	cct	cga	aat	tta	gtt	aaa	tta	tcg	aat	3024
	3529	Gln	Leu	Ile	Ser	Trp	Cys	Asp	Pro	Arg	Asn	Leu	Val	Lys	Leu	Ser	Asn	
W-->	3530					995				1000					1005			
E-->	3532	gag	gaa	ata	aat	caa	gca	aca	tca	cat	tta	tggt	caa	tgt	gtt	tat	tta	3072
	3533	Glu	Glu	Ile	Asn	Gln	Ala	Thr	Ser	His	Leu	Trp	Gln	Cys	Val	Tyr	Leu	
W-->	3534					1010				1015					1020			
E-->	3536	tta	caa	gtg	gtt	gaa	caa	gta	gat	gct	cgt	aat	gtt	aaa	aga	tgc	atc	3120
	3537	Leu	Gln	Val	Val	Glu	Gln	Val	Asp	Ala	Arg	Asn	Val	Lys	Arg	Cys	Ile	
W-->	3538					1025				1030					1035			
E-->	3540	att	aac	aat	ttg	a												

nos.
off

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/786,880

DATE: 08/15/2001

TIME: 08:37:32

Input Set : A:\16655PC1.APP.txt

Output Set: N:\CRF3\08132001\I786880.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1728 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11
M:332 Repeated in SeqNo=11
L:1903 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:1903 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:1903 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1905 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:1905 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:1905 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1907 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:1907 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:1907 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:2219 M:258 W: Mandatory Feature missing, <220> FEATURE: ✓
L:3320 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21
M:332 Repeated in SeqNo=21
L:3484 M:254 E: No. of Bases conflict, LENGTH:Input:2496 Counted:273 SEQ:25
L:3486 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
M:254 Repeated in SeqNo=25
L:3490 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3494 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3498 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3502 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3506 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3510 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3514 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3518 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3522 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3526 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3530 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3534 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3538 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:3540 M:252 E: No. of Seq. differs, <211>LENGTH:Input:231 Found:910 SEQ:25

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<210> 12
<211> 575
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe

<400> 12
gtttggtgac tcaacctacc accaatcgat ttacactctt cataagttct ctagtgtgaa 60
taattgcagg ttgataattt ggtccattg acaataacac tgttgtaagt agctgaaata 120
ttggtacaag gaactcaaaa tatgatatag tgttttctact tcgcaacttg tatggatcca 180
ccaagtcagt tatcgaaagt ggagtatcta gcaaaacatt tacattgaca gtcttgtgat 240
cttgaacttc ttcaattcgt aaacttaaac caatatctgg atcaatctgc aaaaacttcg 300
actgatgcaa aattgaaaac aattcatttt ggaatcannn nnnnaannna aaaaaaatat 360
atattttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 420
aacaccaaac caaaaaaac ccaacacctc catcttgtcc cgctttttctc tcacattttt 480
tctctactac tatcacacaa tctataaaac atacaccccc tcaacccctc ctccccaaca 540
aacctacctc cctcaactcc tatttctctc cttcc 575

See
Item 9
on Ena
Summary
Sheet

FSI

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

<210> 16

<211> 484

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Splice Variant

<400> 16

→ <220> insert this mandatory name
identified

wherever

<221>, <222>,

or <223>

is present